


#5

# FIGURE 1

A. CTIATCGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCAT  
 CACAAATTICACAAATAAGCATTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA  
 ++++++ ↑ ++++++  
 ATGTATCTTATCATGTC (Seq ID NO:1) Cleavage site

B.  AAUAAA  
 ++++++ GCA

C.  GCAaaaaaaaaaaaaaaaaaaaaa (Seq ID NO:18)

+ Upstream and downstream  
 cleavage- polyadenylation elements



# FIGURE 2



## FIGURE 3A

1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGTGAGT  
 +-----ITR-----  
 61 TTGTGACGTGGCGCGGGCGTGGGAACGGGGCGGTGACGTAGGGCGGATCAAGCTTAT  
 +-----ITR-----+ +---  
 121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC  
 -----polyA-----  
 181 ACAAAATTCACAAATAAAGCATTTTTTCTCACTGCATTCTAGTTGTGGTTTGTCCAACTC  
 -----polyA-----  
 241 ATCAATGTATCTTATCATGTCTGGATCCGCGCGCTAGCGATCATCCGACAAAGCCTGC  
 -----+ +-----  
 301 GCGGCCCGCGCCCGCCATTTGGCCGTACCGCGCCCGCGCGCGCCCATCTCGCCCTCG  
 -----E2F-1 promoter-----  
 361 CCGCCGGTCCCGCGCGTTAAAGCCAATAGGAACCGCGCGCTGTTCCTCCGTCACGCGC  
 -----E2F-1 promoter-----  
 421 GGGCAGCCAATTGTGGCGCGCTCGGCGGCTCGTGGCTCTTTCGCGCAAAAAGGATTG  
 -----E2f-1 promoter-----  
 481 GCGCGTAAAGTGGCCGGGACITTTGCAGGCAGCGCGCGCGGGGGCGGAGCGGGATCGAG  
 -----E2f-1 promoter-----  
 541 CCCTCGATGATATCAGATCATCGGATCCCGGTCGACTGAAAATGAGACATATTATCTGCC  
 -----+ +-----  
 601 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAG  
 -----E1a gene-----  
 661 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCITTCACGAAGTG  
 -----E1a gene-----  
 721 ATGATTTAGACGTACCGCCCCGAAGATCCCAACGAGGAGCGGTTTCGAGATTTTC  
 -----E1a gene-----  
 781 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTTCGCGCGCGC  
 -----E1a gene-----  
 841 CCGGTTCTCCGGAGCCCGCTCACCTTTCCCGGCAGCCCGAGCAGCCGAGCAGAGAGCCT  
 -----E1a gene-----  
 901 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGG  
 -----E1a gene-----



# FIGURE 3B

```

961 CTGGCTTTCCACCCAGTGAACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
-----E1a gene-----
1021 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCAATTATCACCGGAGGAATACGGGGGACC
-----E1a gene-----
1081 CAGATATTATGTGTTGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
-----E1a gene-----
1141 GAAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTGGTGTGGTAATTTTTTTTTTAAT
-----E1a gene-----
1201 TTTTACAGTTTGTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC
-----E1a gene-----
1261 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA
-----E1a gene-----
1321 AATGGCGCCTGCTATCCTGAGACGCCCCGACATCACTGTGTCTAGAGAATGCAATAGTAG
-----E1a gene-----
1381 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC
-----E1a gene-----
1441 GCTGTGCCCCATTAAACCAAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG
-----E1a gene-----
1501 TATCGAGGACTTGCTTAAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAACGCCCCAG
-----E1a gene-----
1561 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCCTTTGTTTGCTGAATGAGT
-----E1a gene-----
1621 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTAAATGGGGC
-----+-----
1681 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAACTTTGGTTACATCTGACCTCATGGA
-----E1b gene-----
1741 GGCTTGGGAGTGTTTGAAGATTTTTCTGCTGTGCGTAACCTTGCTGGAACAGAGCTCTAA
-----E1b gene-----
1801 CA
--

```



## FIGURE 3C

33881 AACCTACGCCAGAAACGAAAGCCAAAAACCCACAACCTTCTCAAATCGTCACCTCCGT

33941 TTTCCACGTTACGTCACTTCCCATTTTAAATTAAGAATTCTACAATTCCCAACACATACA

34001 AGTTACTCGCCCTAAAAACCTGGGCGAGTCTCCACGTAAACGGTCAAAGTCCCCGCGGC  
+--packaging signal-----

34061 CCTAGACAAATATTACGCGCTATGAGTAACACAAAATTATTCAGATTTCACTTCCTCTTA  
-----packaging signal-----

34121 TTCAGTTTTCCTCGGAAAAATGGCCAAATCTTACTCGGTTACGCCCAAATTTACTACAACA  
-----packaging signal-----

34181 TCCGCCTAAAACCGCGCGAAAAATTGTCACTTCCTGTGTACACCGCGCACACCAAAAACG  
-----+-----

34241 TCACTTTTGCCACATCCGTGCTTACATGTGTTCCGCCACACTTGCAACATCACACTTCC

34301 GCCACACTACTACGTACCCCGCCCCGTTCACGCCCCCGCGCCACGTACAAAACCTCCACC  
+-----ITR-----

34361 CCCTCATTATCATATTGGCTTCAATCCAAAATAAGGTATATTATTGATGATG  
-----ITR-----+



# FIGURE 4

```

1  CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
   +-----ITR-----

61  TTGTGACGTGGCGCGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGCCGCTAGCGAT
   -----ITR-----++-----MCS-----

121 ATCGGATCCCGGTCGACTGAAAATGAGACATATATCTGCCACGGAGGTGTATTACCGA
   -----+-----E1a-----

181 AGAAATGGCCGCAGTCTTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCC
   -----E1a-----

241 ACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACGTATGATTAGACGTGACGGC
   -----E1a-----

301 CCCCAGAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGC
   -----E1a-----

361 GGTGCAGGAAGGGATTGACTTACTCACTTTTCGCGCGCGCCCGGTTCTCCGAGCGCGC
   -----E1a-----

421 TCACCTTTCCCGGCAGCCCGAGCAGCCGAGCAGAGACCTTGGGTCCGGTTTCTATGCC
   -----E1a-----

481 AAACCTTGTAACCGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGA
   -----E1a-----

541 CGACGAGGATGAAGAGGGTGAGGAGTTTGTGTAGATTATGTGGAGCACCCCGGCACGG
   -----E1a-----

601 TTGCAAGTCTTGTCATTATACCGGAGGAATACGGGGACCCAGATATTATGTGTTGCT
   -----E1a-----

```



## FIGURE 5

```

1  CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
   +-----ITR-----
61  TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
   -----ITR-----+-----
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
   -----polyA-----
181 ACAAATTTCACAAATAAAGCATTTTTTCACCTGCATCTAGTTGTGGTTTGTCCAAACTC
   -----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATATCGGATCCCGGTCGACT
   -----+-----
301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCT
   -----Ela-----
361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGA
   -----Ela-----
421 ACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGA
   -----Ela-----
481 GGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGA
   -----Ela-----
541 CTTACTCACTTTTCCGCGGCGCCGGTTCTCCGAGCGCGCTCACCTTCCCGGCAGCC
   -----Ela-----
601 CGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTAACCGGAGGT
   -----Ela-----

```



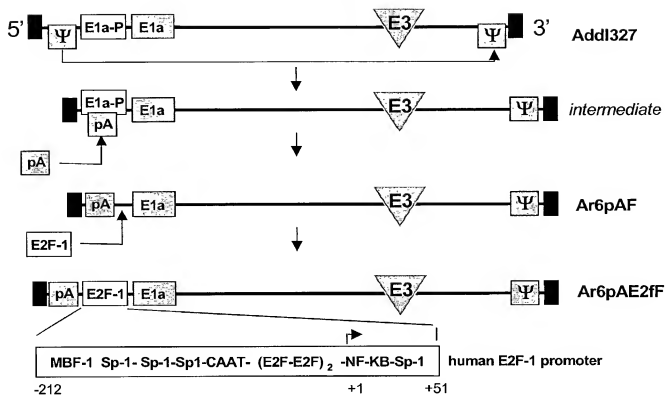


FIGURE 6





Fig. 7 Body weight change

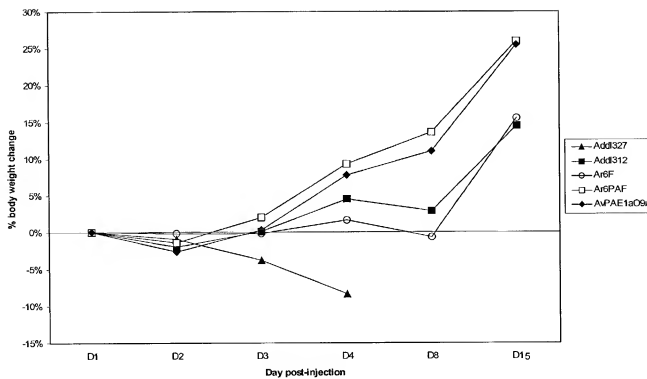


Fig. 8 Minimizing nonspecific transactivation of E1a gene

Backbones generated:

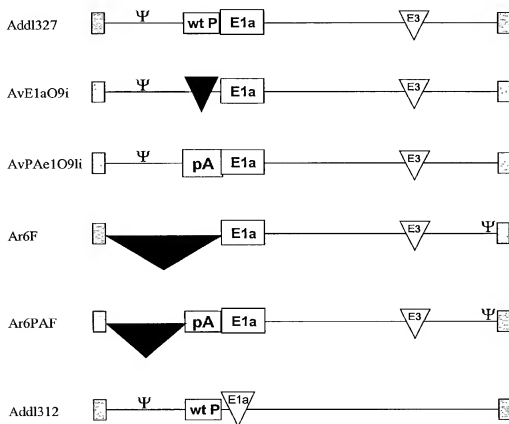


Figure 9. Mean H460 tumor volume

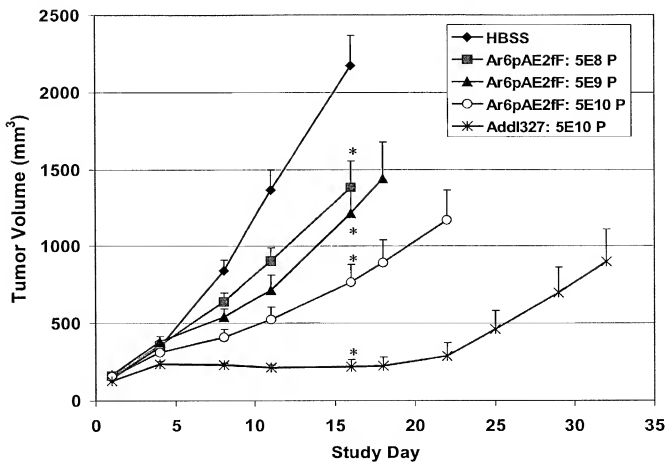


FIGURE 10

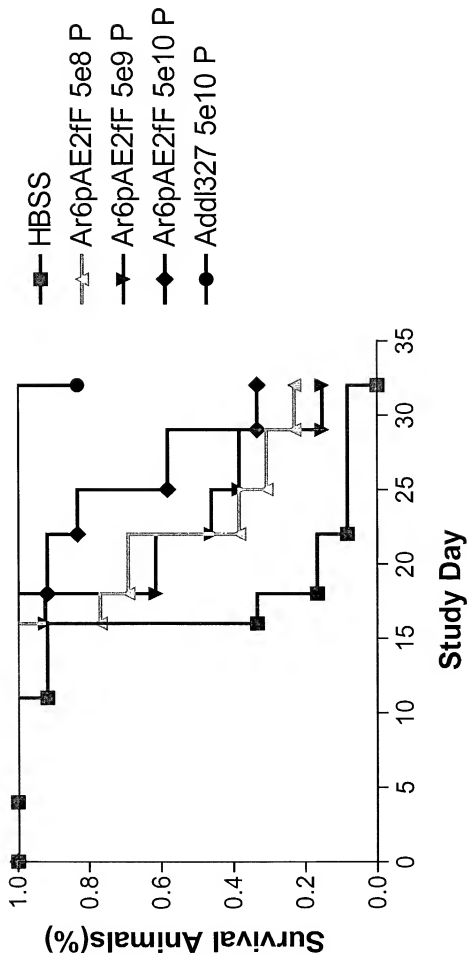


FIGURE 11

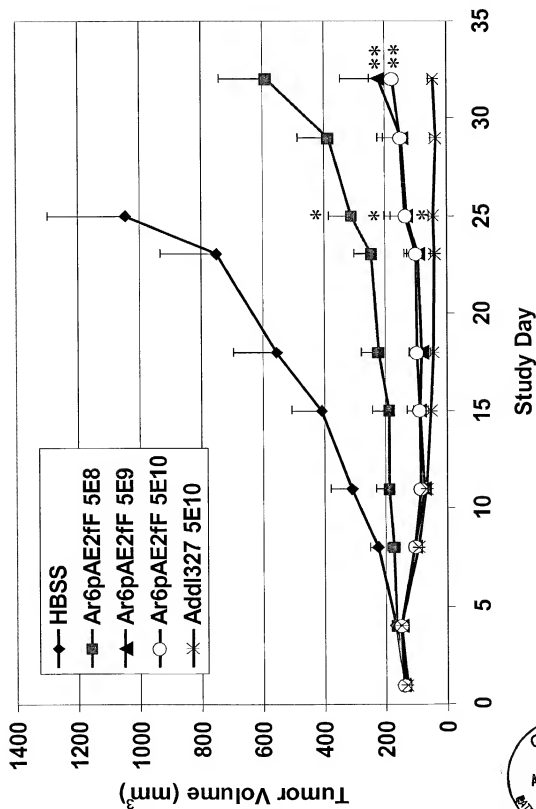


Figure 1 is a Kaplan-Meier survival plot showing Percent Survival (Y-axis, 0 to 100) versus Time (Days) (X-axis, 0 to 40). The plot compares the survival of five groups: HBSS (dashed line with open squares), Ar6pAE2fF 5E8 (solid line with open squares), Ar6pAE2fF 5E9 (solid line with open triangles), Ar6pAE2fF 5E10 (solid line with diamonds), and Addl327 5E10 (solid line with solid circles). The HBSS group shows the highest survival, remaining at 100% until day 25, then dropping to approximately 80% at day 30 and 60% at day 35. The other four groups show a rapid decline in survival, reaching approximately 50% survival by day 10 and remaining stable thereafter.

Time (Days)	HBSS	Ar6pAE2fF 5E8	Ar6pAE2fF 5E9	Ar6pAE2fF 5E10	Addl327 5E10
0	100	100	100	100	100
5	100	100	100	100	100
10	100	50	50	50	50
25	100	50	50	50	50
30	80	50	50	50	50
35	60	50	50	50	50

FIGURE 13

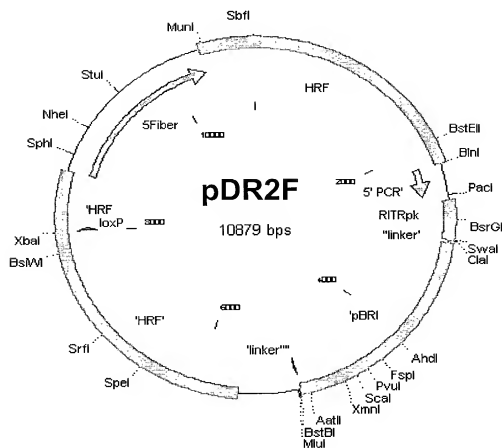


FIGURE 14

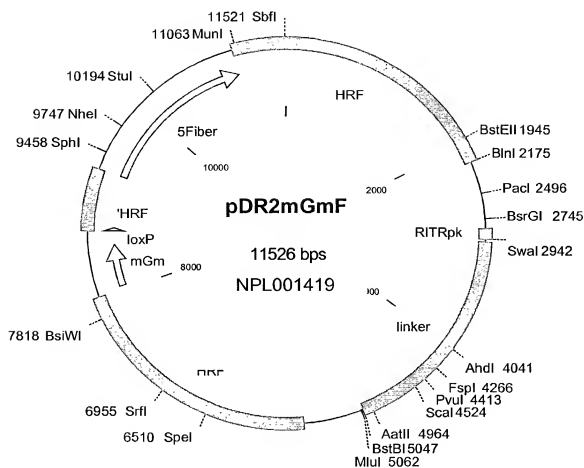




FIGURE 15

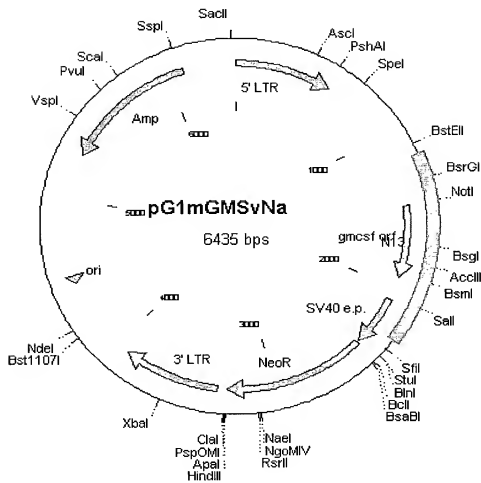


FIGURE 16

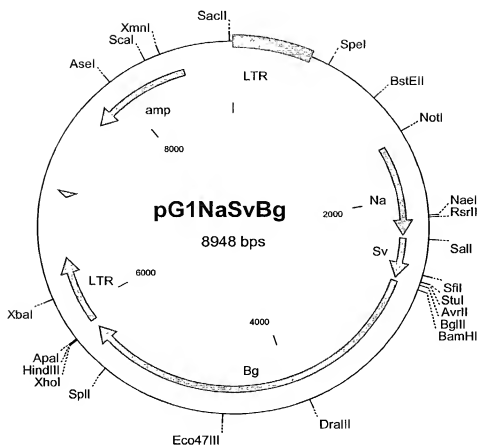


FIGURE 17

7878 TTCCGGACAG ACCTCAATAA CTCTGTTTAC CAGAACAGGA GGTGAGCTTA  
7928 GAAAACCCCTT AGGGTATTAG GCCAAAGGCG CAGCTACTGT GGGGTTTATG  
7978 AACCAATTCAA GCAACTCTAC GGGCTATTCT AATTCAGGTT TCTCTAGCCG  
8028 GGCTGCAGGA ATTCGATGGC CGTACCTTAC AATGGCCCCAC GAGAGAAAGG  
M A H E R K  
8078 CTAAGGTCCT GAGGAGGATG TGGCTGCAGA ATTTACTTTT CCTGGGCATT  
A K V L R R M W L Q N L L F L G I  
8128 GTGGTCTACA GCCTCTCAGC ACCCACCCTG TCACCCATCA CTGTCACCCG  
V V Y S L S A P T R S P I T V T  
8178 GCCTTGGAAG CATGTAGAGG CCATCAAAGA AGCCCTGAAC CTCCTGGATG  
R P W K H V E A I K E A L N L L D  
8228 ACATGCCTGT CACATTGAAT GAAGAGGTAG AAGTCGTCTC TAACGAGTTC  
D M P V T L N E E V E V V S N E F  
8278 TCCTTCAAGA AGCTAACATG TGTGCAGACC CGCCTGAAGA TATTCGAGCA  
S F K K L T C V Q T R L K I F E  
8328 GGGTCTACGG GGCAATTTCA CCAAACTCAA GGGCGCCTTG AACATGACAG  
Q G L R G N F T K L K G A L N M T  
8378 CCAGCTACTA CCAGACATAC TGCCCCCAA CTCCGGAAAC GGA CTGTGAA  
A S Y Y Q T Y C P P T P E T D C E  
8428 ACACAAGTTA CCACCTATGC GGATTTCATA GACAGCCTTA AAACCTTTCT  
T Q V T T Y A D F I D S L K T F  
8478 GACTGATATC CCCTTTGAAT GCAAAAAACC AGTCCAAAAA TGAGGAAGCC  
L T D I P F E C K K P V Q K -  
8528 CAGGCCAGCT CTGAATCCAG CTTCTCAGAC TGCTGCTTTT GTGCCTGCGT  
8578 AATGAGCCAG GAACTCGGAA TTTCTGCCTT AAAGGGACCA AGAGATGTGG  
8628 CACAGGTAGT CGAATCAAGC TTATCGATAC CGTCGACCTC GACTAGATAA  
8678 CTTTCGTATA TGTATGCTAT ACGAAGTTAT GCTAGAAATG GACGGAATTA  
8728 TTACAGAGCA GCGCCTGCTA GAAAGACGCA GGGCAGCGGC CGAGCAACAG  
8778 CGCATGAATC AAGAGCTCCA AGACATGGTT AACTTGCACC AGTGCAAAA 8826



FIGURE 18

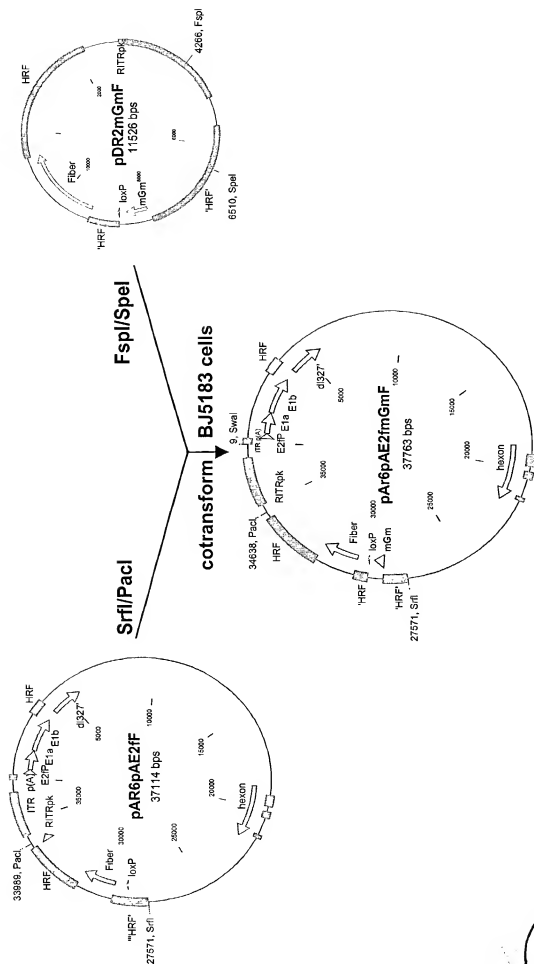
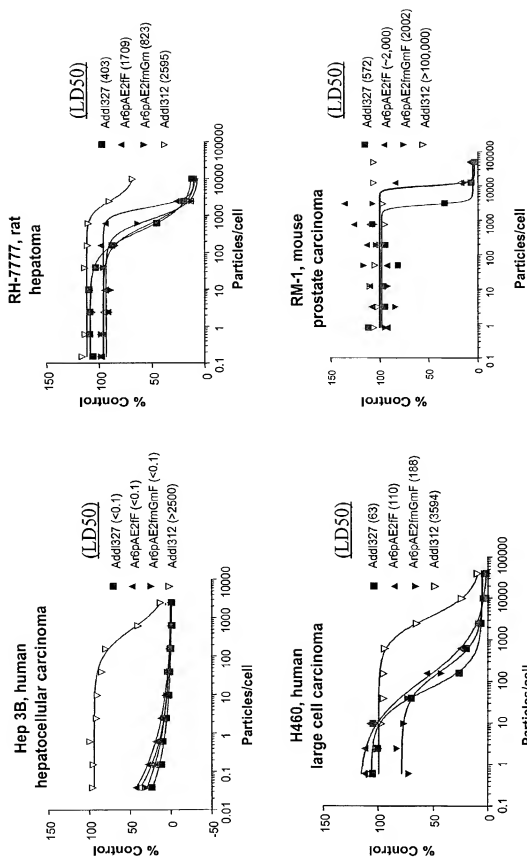


FIGURE 19





## FIGURE 21

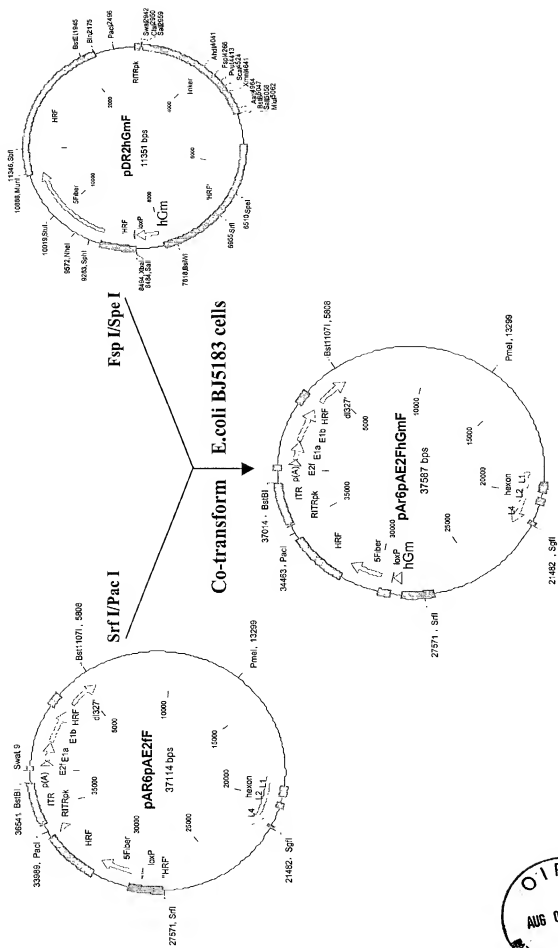


FIGURE 22

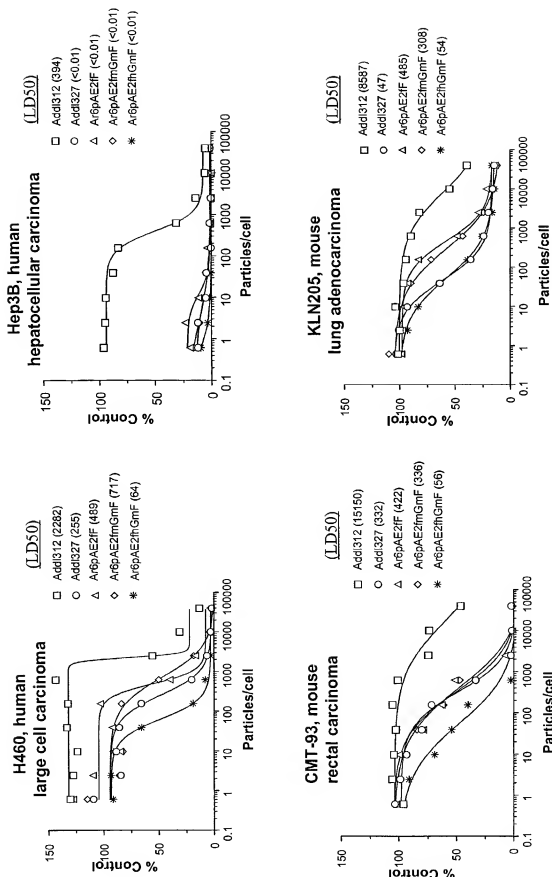




FIGURE 23

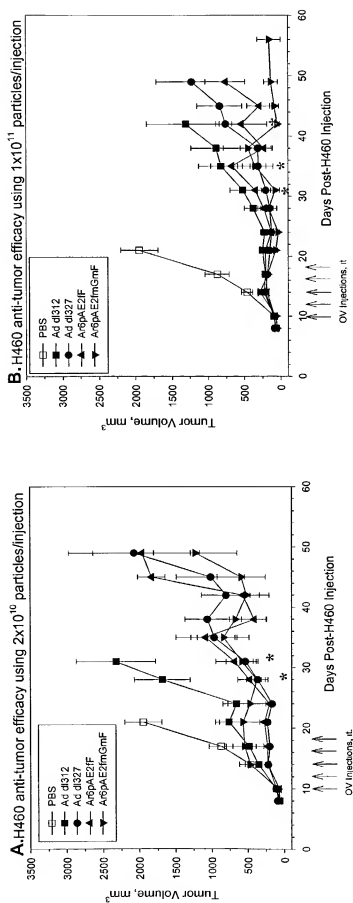


FIGURE 24

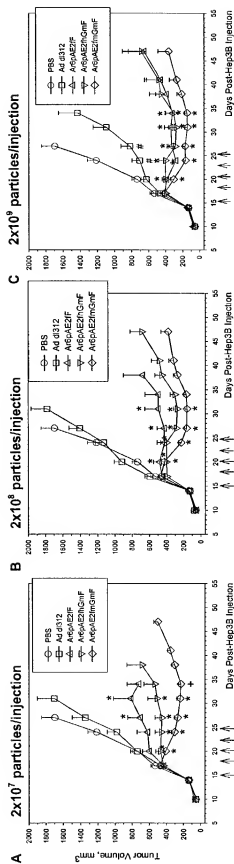
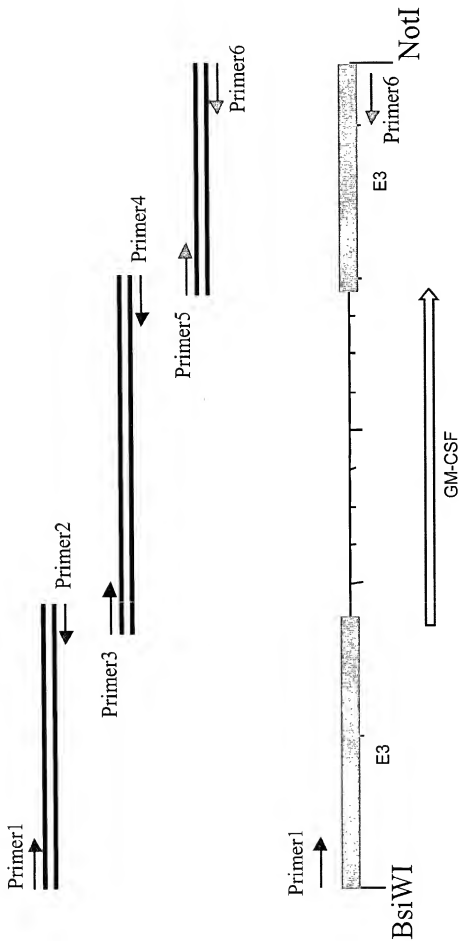
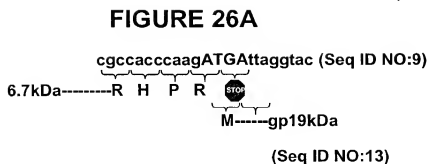


FIGURE 25





**FIGURE 26B**

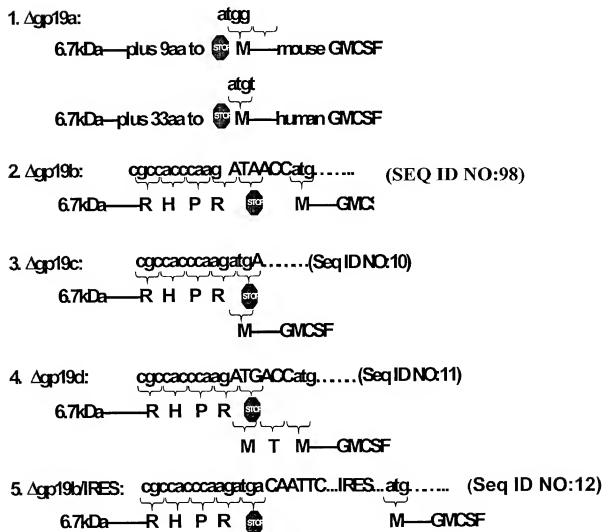


FIGURE 27A

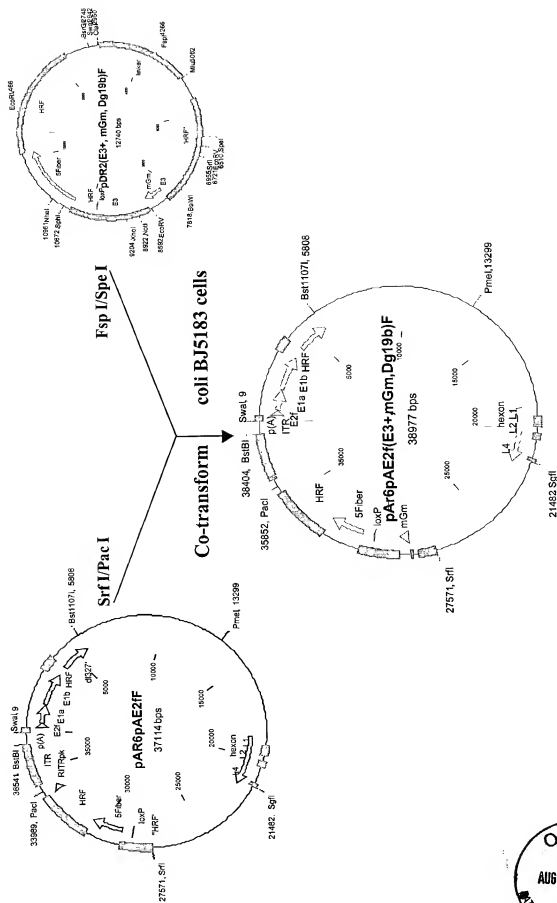


FIGURE 27B

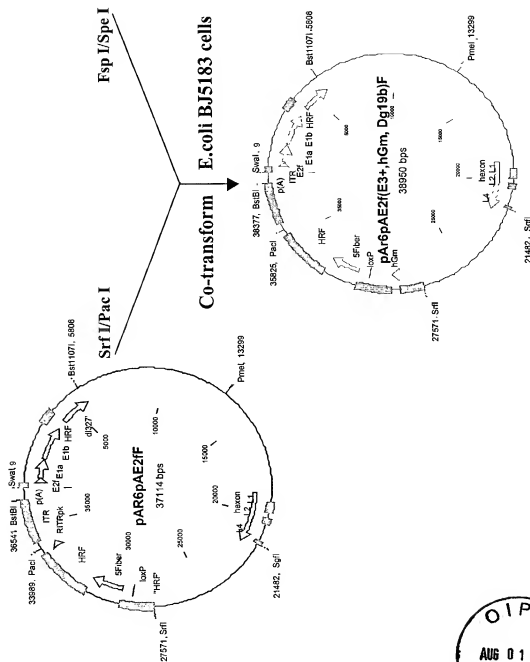
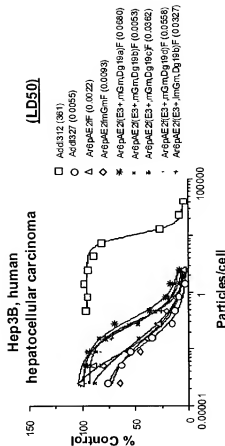
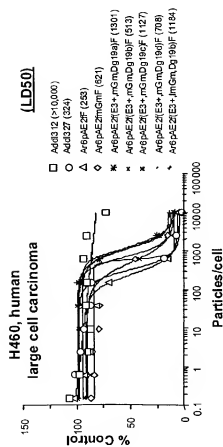
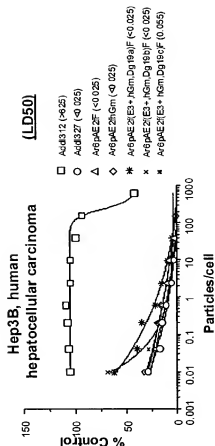
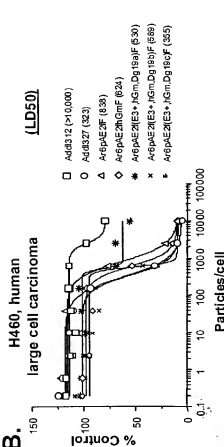


FIGURE 28

A.



B.



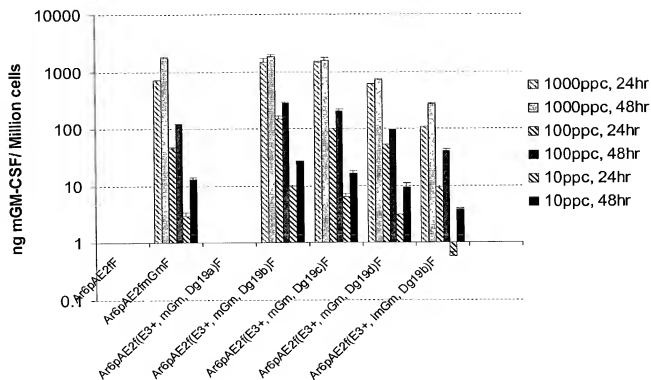
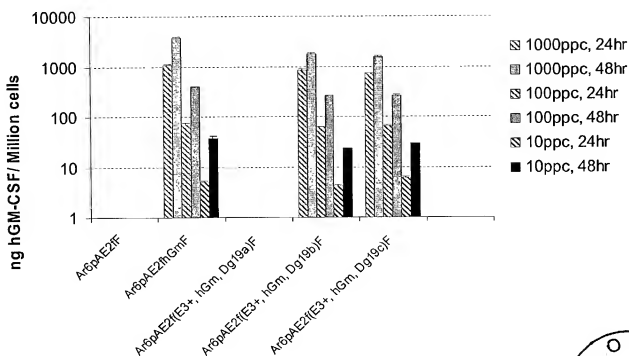
**Figure 29****a. Mouse GM-CSF expression in H460 cells****b. Human GM-CSF expression in H460 cells**



Figure 30

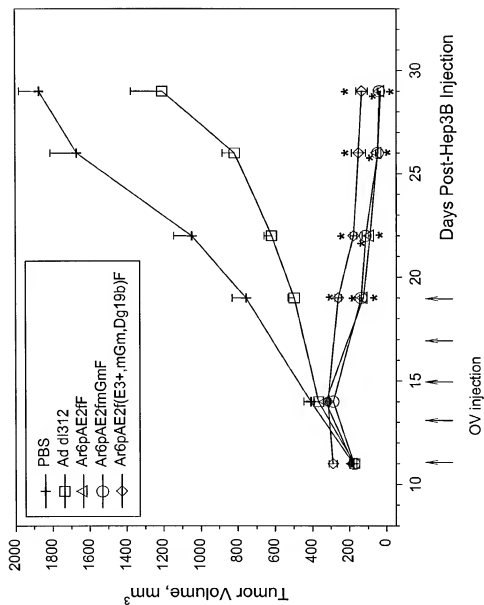
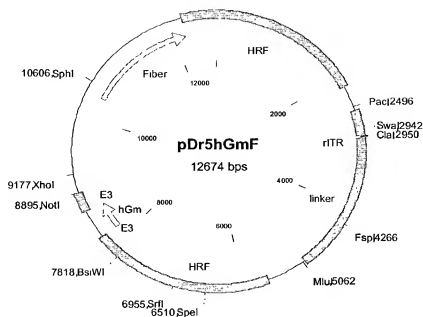


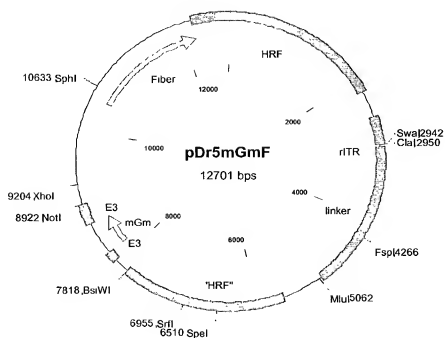


Figure 32

A. pDr5hGmF



B. pDr5mGmF



Co-transform	E. coli BJ5183 cells
+	+
-	-

The diagram illustrates the genetic constructs and transformation strategy for *E. coli* BJ5183 cells. Three circular plasmids are shown:

- pAR6pAE2F (17714 bps):** Contains genes for tetracycline resistance (*TetR*), ampicillin resistance (*AmpR*), and a Shine-Dalgarno sequence (*SD*). It also includes a *lacZ* gene and a *lacI* gene.
- pAR15pAE2fGmF (38938 bps):** Contains genes for tetracycline resistance (*TetR*), ampicillin resistance (*AmpR*), and a Shine-Dalgarno sequence (*SD*). It also includes a *lacZ* gene and a *lacI* gene.
- pD5mGmF (12701 bps):** Contains genes for tetracycline resistance (*TetR*), ampicillin resistance (*AmpR*), and a Shine-Dalgarno sequence (*SD*). It also includes a *lacZ* gene and a *lacI* gene.

The transformation strategy involves co-transforming *E. coli* BJ5183 cells with the pAR6pAE2F and pAR15pAE2fGmF plasmids, followed by selection on tetracycline and ampicillin. The resulting transformants are then screened for the presence of the pD5mGmF plasmid.

Figure 35

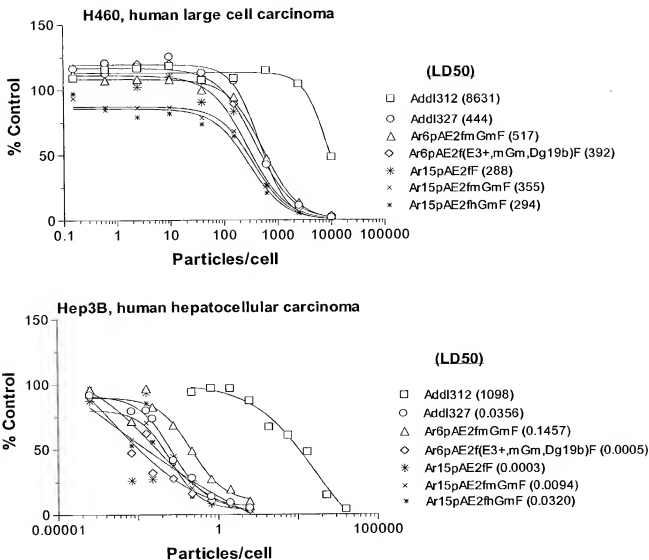


Figure 36

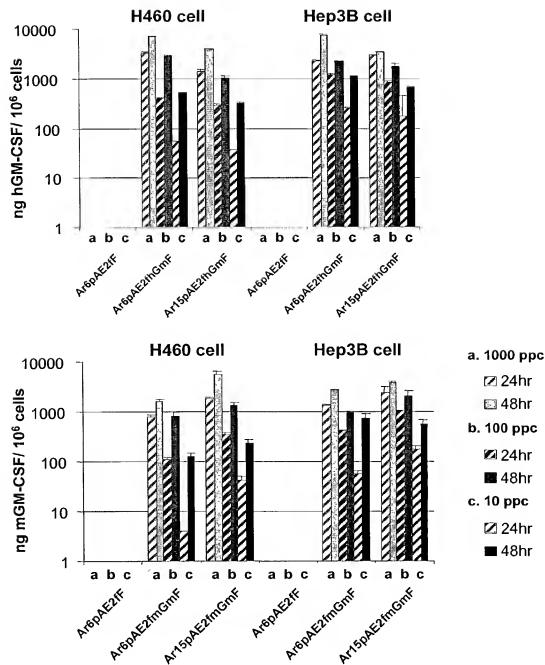


Figure 37

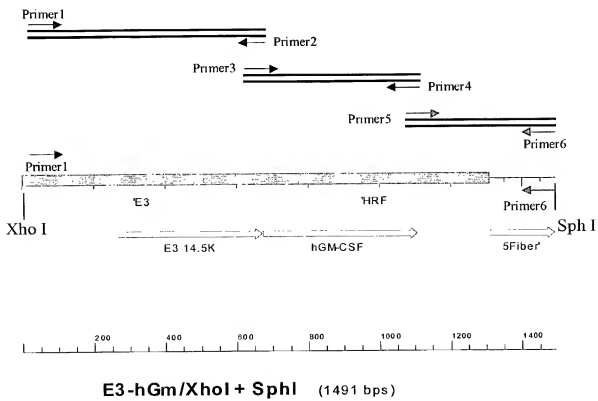
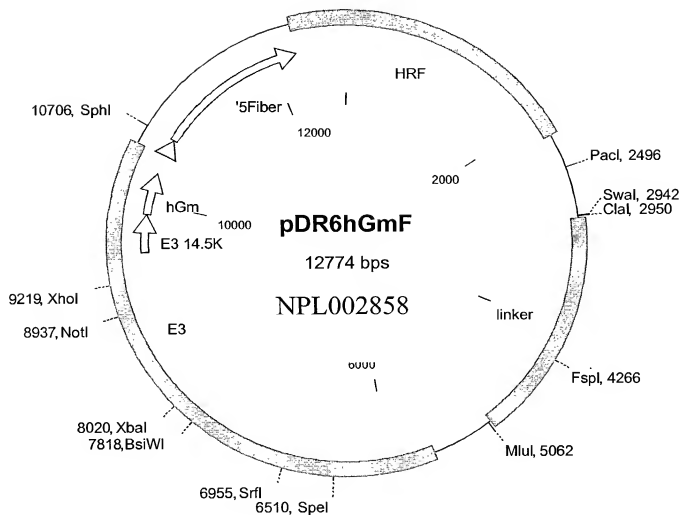






Figure 39





## Figure 41

## H460, human large cell carcinoma

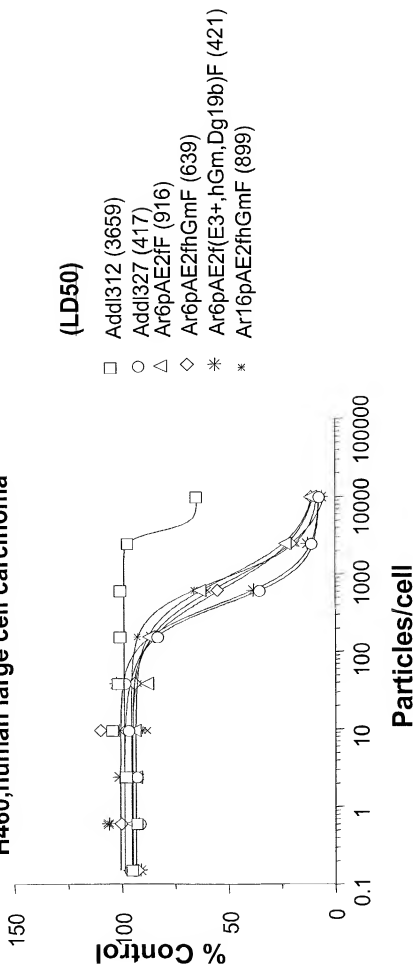


Figure 42

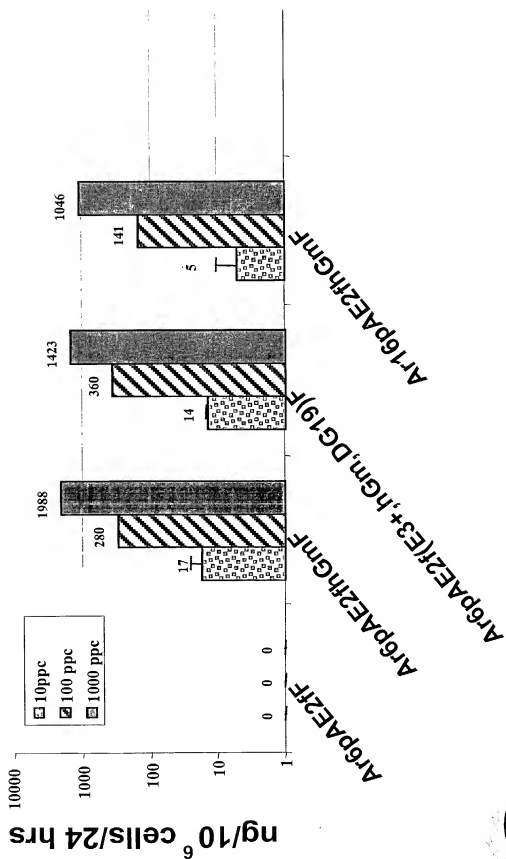
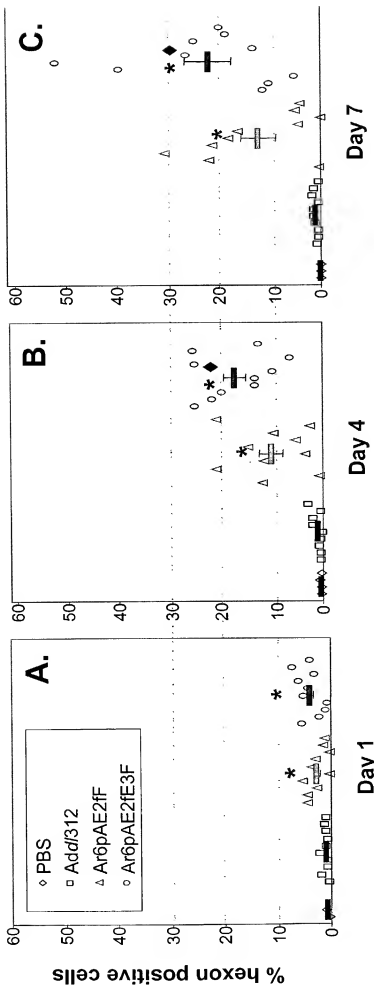


Figure 43

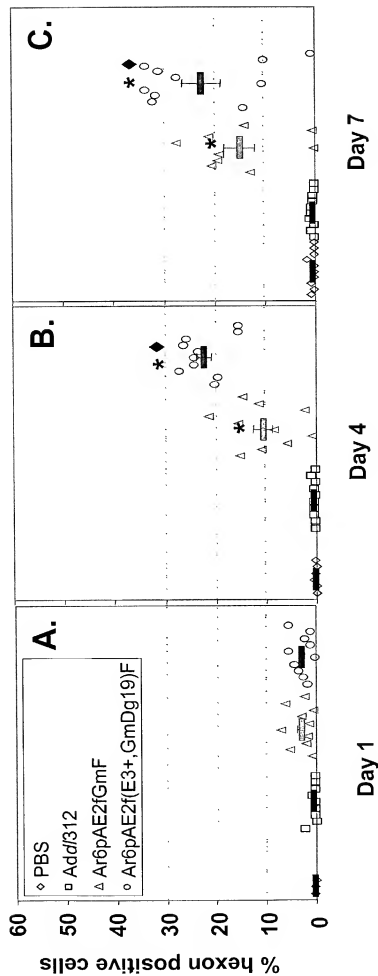


\*:  $p < 0.05$  between Ar6pAE2fF or Ar6pAE2fE3F and Add/312, ANOVA

\*:  $p < 0.05$  between Ar6pAE2fF and Ar6pAE2fE3F vectors, ANOVA



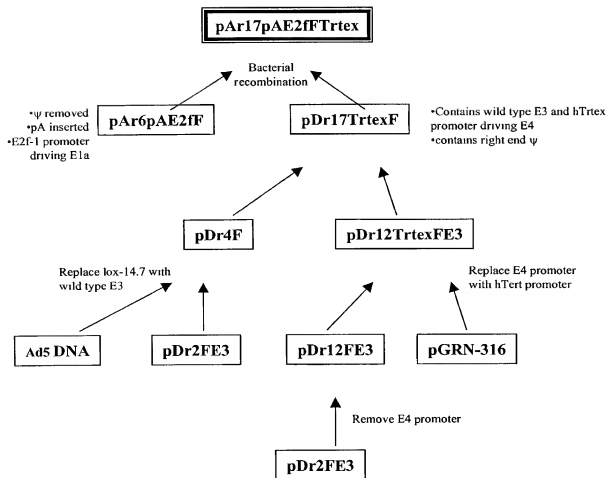
Figure 44



\*: p < 0.05 between Ar6pAE2f(E3+, hGm, Dg19)F and Add/312, ANOVA  
 \*: p < 0.05 between Ar6pAE2f(E3+, hGm, Dg19)F vectors, ANOVA



Figure 45





The figure displays two circular plasmid maps. The top map is for the **A17pAE2/Flrtex** plasmid, which is 36305 bps. It features a large **hrf** gene, a **fiber** gene, and a **hsdR** gene. Restriction sites include *PacI*, *EcoRI*, *HindIII*, *SfiI*, *SpeI*, *SphI*, *NheI*, and *SmaI*. The bottom map is for the **pDR17trtEx** plasmid, which is 12770 bps. It features a **hrf** gene, a **fiber** gene, and a **hsdR** gene. Restriction sites include *AatII*, *XmaI*, *SmaI*, *PacI*, *FspI*, *AhaI*, *RITRok*, *BamHI*, *FspI*, *BstEII*, *SfiI*, *SphI*, *NheI*, and *SmaI*. Both maps also show the **htrEG** promoter and a **linker** region.

Figure 47

```

35351 agtgctaaaa agcgaccgaa atagcccggg ggaatacata cccgcaggcg
35401 tagagacaac attacagccc ccataggagg tataacaaaa ttaataggag
35451 agaaaaacac ataaacacct gaaaaacct cctgcctagg caaaatagca
35501 ccctcccgct ccagaacaac atacagcgct tcacagcggc agcctaacag
35551 tcagccttac cagtaaaaaa gaaaacctat taaaaaaaca ccactcggat
35601 caattcgcgg ggggtggcgg ggccagggct tcccacgtgc gcagcaggac
35651 gcagcgctgc ctgaaactcg cgcgcgagg agagggcggg gccgcggaaa
35701 ggaaggggag gggctgggag ggcccgagg gggctgggcc ggggacccgg
35751 gaggggtcgg gacggggcgg ggtccgcgcg gaggaggcgg agctggaagg
35801 tgaaggggca ggacgggtgc cgggtcccc agtccctccg ccacgtgggg
35851 ctaggatcct taattaagaa ttctacaatt cccaacacat acaagtact
35901 ccgccctaaa accctgggcg agtctccacg taaacggtca aagtccccgc
35951 ggccttagac aaatattacg cgctatgagt aacacaaaat tattcagatt
36001 tcacttcctc ttattcagtt ttcccgcaa aatggccaaa tcttactcgg
36051 ttacgcccac atttactaca acatccgcct aaaaccgcgc gaaaattgtc
36101 acttcctgtg tacaccggcg cacaccaaaa acgtcacttt tgccacatcc
36151 gtgcgttaca tgtgttccgc cacacttgca acatcacact tcgcgcacac
36201 tactacgtca cccgccccgt tcccacgcc cgcgccacgt cacaaactcc
36251 accccctcat tatcatattg gcttcaatcc aaaataaggt atattattga
36301 tgatg

```



**Figure 48**

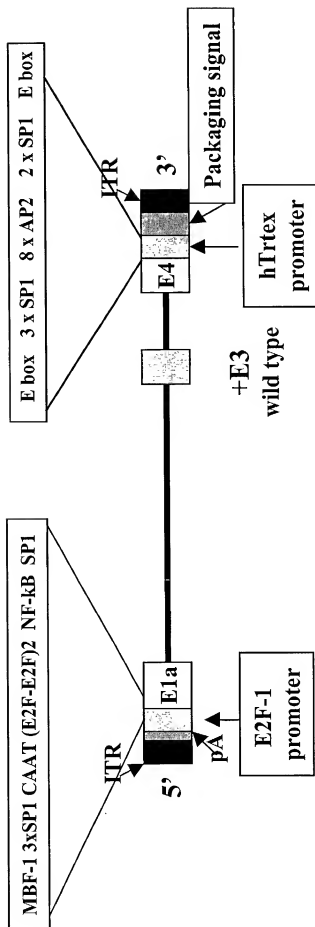
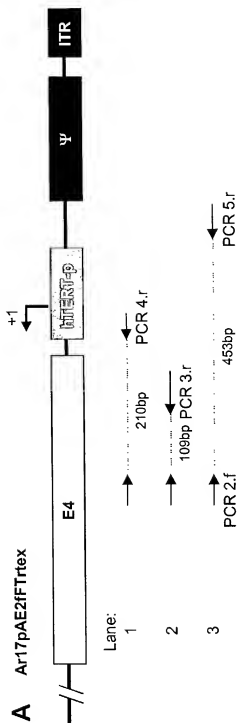


Figure 49



[illegible]

Figure 51

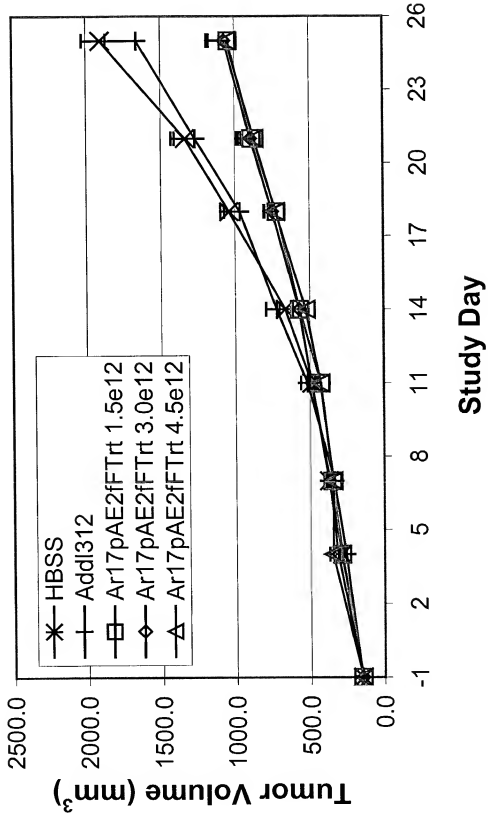


Figure 52

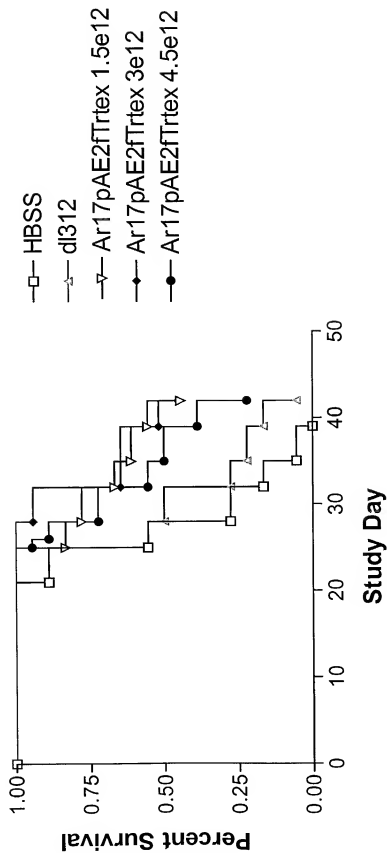


Figure 53

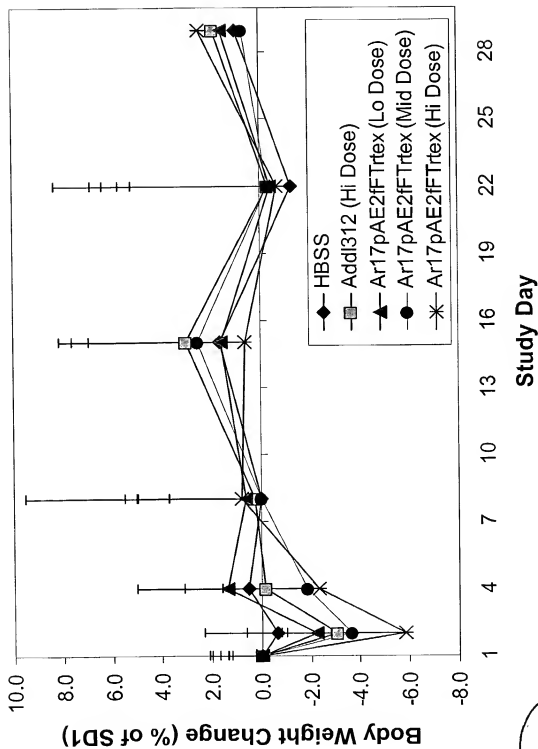




Figure 54

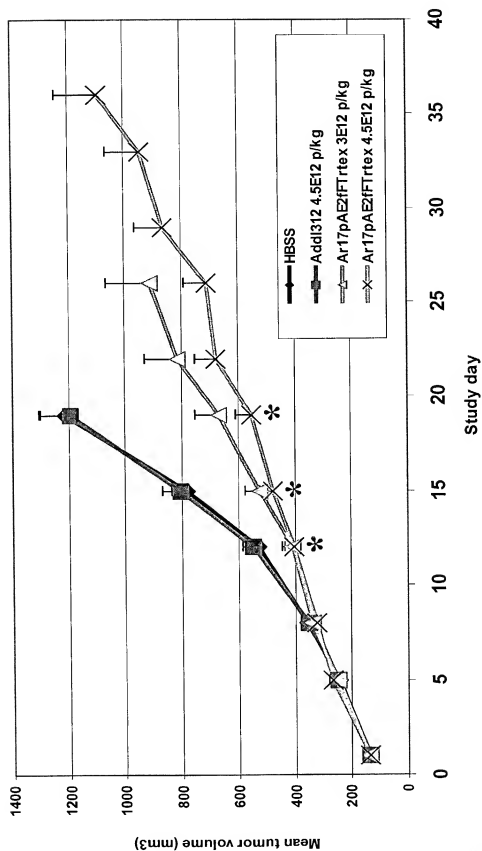
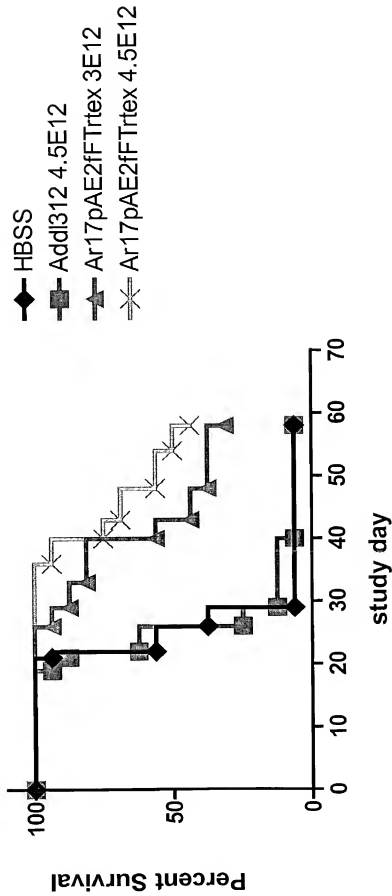


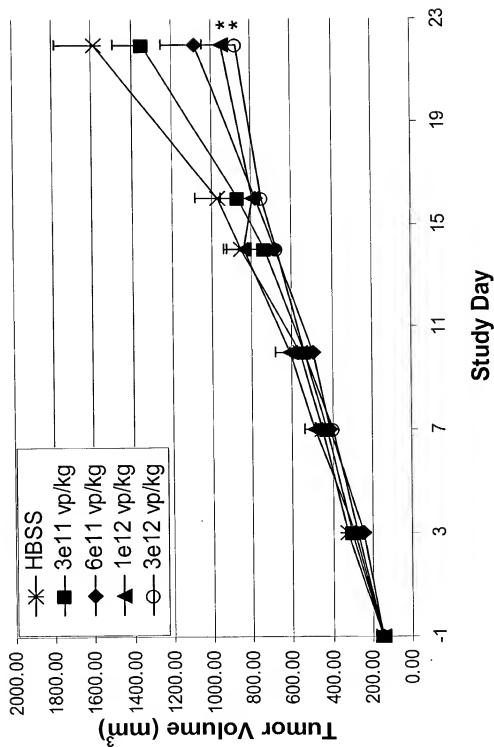
Figure 55



1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26



Figure 57



**Figure 58**

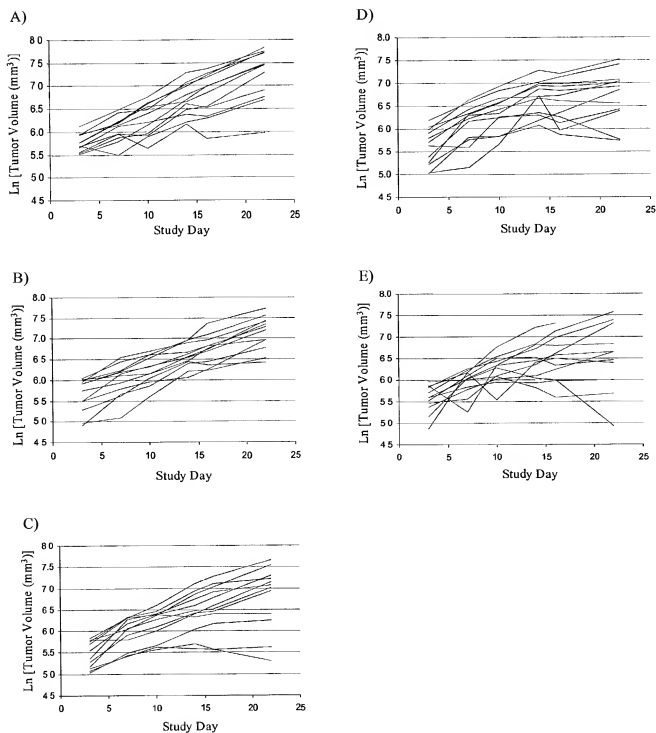


Figure 59

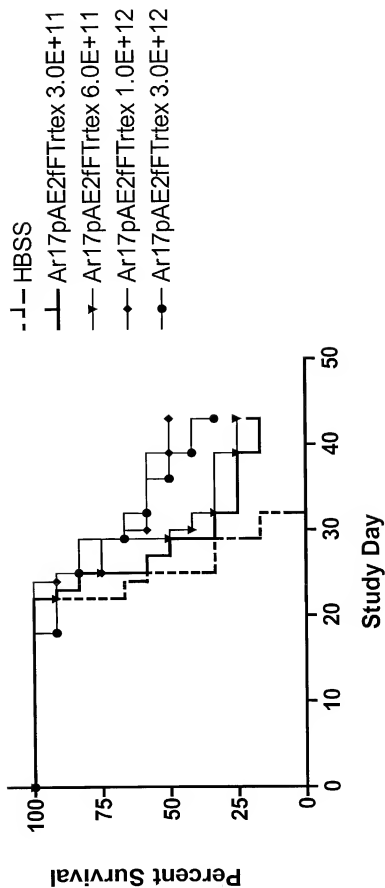


Figure 60

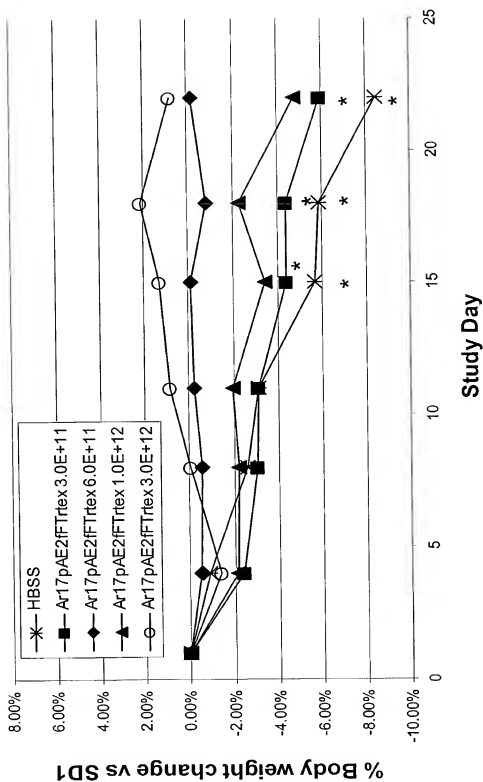


Figure 61

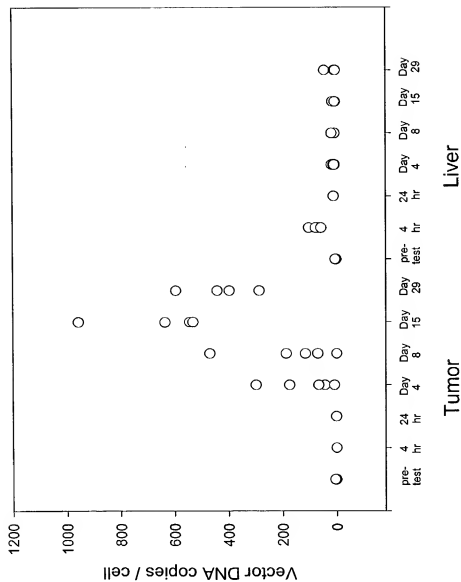




Figure 62

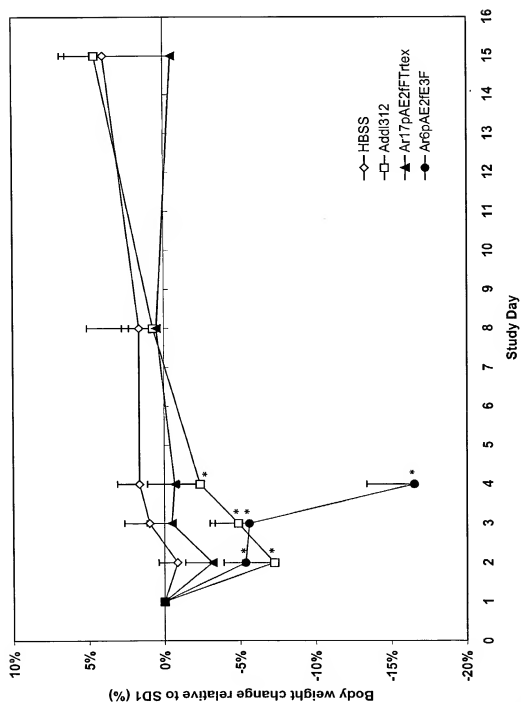
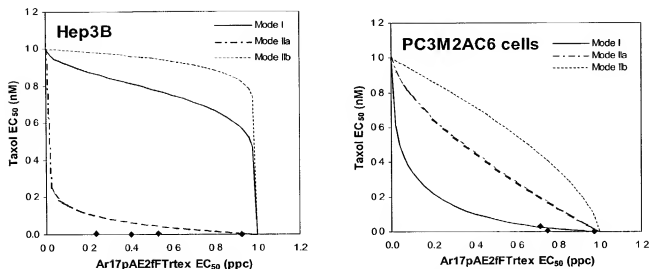


FIGURE 63

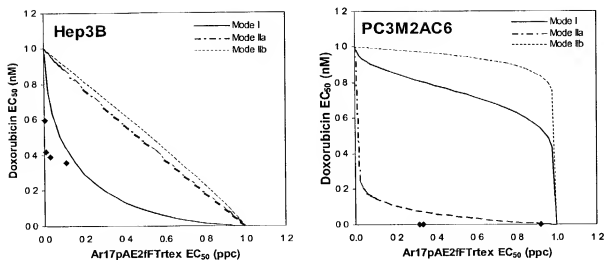


MR (ppc/nM)	Virus EC <sub>50</sub> <sup>b</sup>	Chemo EC <sub>50</sub> <sup>b</sup>	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
8.3e-05	0.23	0.0043	synergy
3.3e-04	0.53	0.0024	synergy
1.3e-03	0.40	0.00046	synergy
5.3e-03	0.93	0.00027	synergy

MR (ppc/nM)	Virus EC <sub>50</sub> <sup>b</sup>	Chemo EC <sub>50</sub> <sup>b</sup>	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
0.02	3.4	1.3	antagonism
0.2	0.71	0.028	synergy
2	0.75	0.003	synergy
20	0.97	0.0004	synergy



Figure 64



MR (ppc/nM)	Virus EC <sub>50</sub> <sup>b</sup>	Chemo EC <sub>50</sub> <sup>b</sup>	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
1.3e-05	0.0028	0.60	synergy
5.0e-05	0.0078	0.42	synergy
2.0e-04	0.029	0.39	synergy
8.0e-04	0.11	0.36	synergy

MR (ppc/nM)	Virus EC <sub>50</sub> <sup>b</sup>	Chemo EC <sub>50</sub> <sup>b</sup>	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
1	2.2	0.015	antagonism
10	0.92	6.1e-4	synergy
100	0.34	2.2e-5	synergy
1000	0.32	2.1e-6	synergy





Figure 66

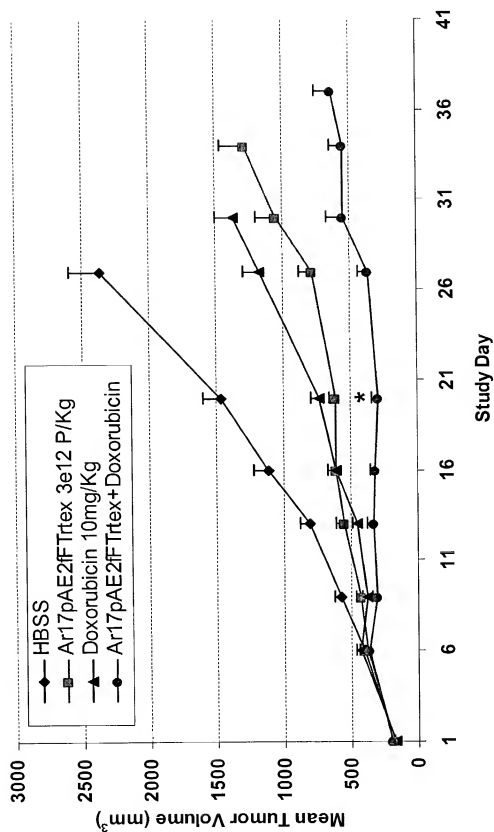


Figure 67

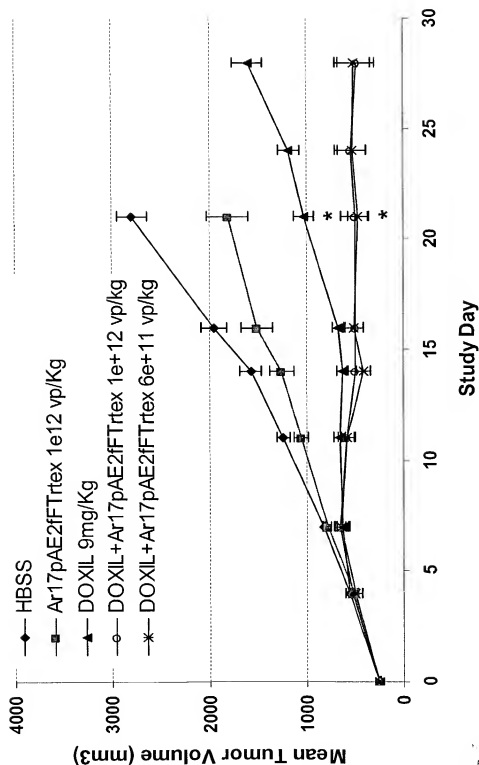


Figure 68

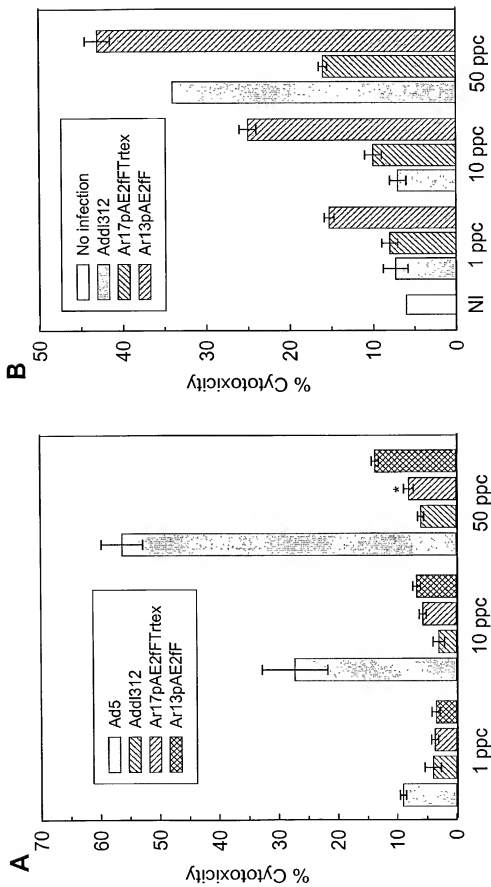
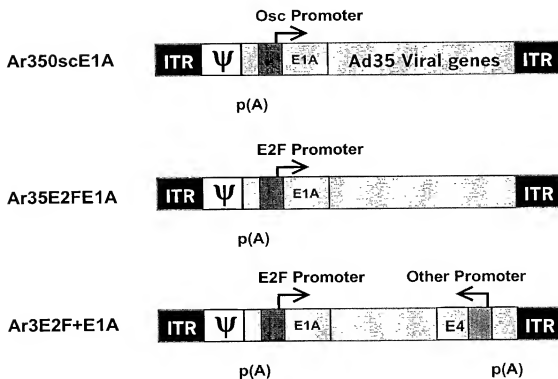


Figure 69

# Ad35-Based Oncolytic Vectors





## Figure 70

